

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/516, 768  
Source: PCT  
Date Processed by STIC: 06/15/2005

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PCT

## RAW SEQUENCE LISTING

DATE: 06/15/2005

PATENT APPLICATION: US/10/516,768

TIME: 14:43:37

Input Set : A:\62273715.app

Output Set: N:\CRF4\06152005\J516768.raw

3 <110> APPLICANT: MINAMINO, NAOTO  
 4 KATAFUCHI, TAKESHI  
 6 <120> TITLE OF INVENTION: NOVEL PEPTIDES HAVING cAMP PRODUCING ACTIVITY  
 8 <130> FILE REFERENCE: 62273(71526)  
 10 <140> CURRENT APPLICATION NUMBER: 10/516,768  
 11 <141> CURRENT FILING DATE: 2004-12-03  
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/06641  
 14 <151> PRIOR FILING DATE: 2003-05-28  
 16 <150> PRIOR APPLICATION NUMBER: JP 2002-162797  
 17 <151> PRIOR FILING DATE: 2002-06-04  
 19 <160> NUMBER OF SEQ ID NOS: 52  
 21 <170> SOFTWARE: PatentIn Ver. 3.3  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 38  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Sus sp.  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: C-term may be amidated  
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 33 1 5 10 15  
 35 Ser Arg Ser Gly Ser Met Val Arg Ser Asn Leu Leu Pro Thr Lys Met  
 36 20 25 30  
 38 Gly Phe Lys Val Phe Gly  
 39 35  
 42 <210> SEQ ID NO: 2  
 43 <211> LENGTH: 39  
 44 <212> TYPE: PRT  
 45 <213> ORGANISM: Sus sp.  
 47 <400> SEQUENCE: 2  
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 54 Gly Phe Lys Val Phe Gly Gly  
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 60 <212> TYPE: DNA  
 61 <213> ORGANISM: Sus sp.  
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 65 gctccctct ctgctccagt ccacctgggt cctgctgccc gaggggcacc atgggcttct 120

CP5.6)

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66 ggaaatttcc gcccttctcg gttctcagca tcctgggtcct gtaccaggca ggcattgttcc 180
67 acacagcacc aatgaggtct gcctttggga gcccttttga tcctgctacc ctctctgagg 240
68 aggaatcacg cctccttttg gctgcaatgg tgaatgacta tgagcagatg aaggcccggtg 300
69 agatgcagaa gcagagggca cagggctccg gcatcagtgt ccagaagaga tcctgcaaca 360
70 ctgccacctg catgacccat cggctggtgg gcttgctcag cagatctggg agcatggtga 420
71 ggagcaacct gttgccacc aagatgggct tcaaagtctt tgggtgggcgc cgcaggaact 480
72 tttggatctg agcagtggga tgattccagg aggaagggtta ctatgactct gaactctatt 540
73 cgtttaattt acaatgaaag caacctacta aaaaatagca tggaagacat ccatgtatgc 600
74 atgcttctgg aaactgaaaa cactcttttc cttgaaataa actaaaacta aatgcaaaat 660
75 aaaatcaatg catcaatgc                                     679
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80 <212> TYPE: PRT
81 <213> ORGANISM: Sus sp.
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87 Leu Tyr Gln Ala Gly Met Phe His Thr Ala Pro Met Arg Ser Ala Phe
88           20           25           30
90 Gly Ser Pro Phe Asp Pro Ala Thr Leu Ser Glu Glu Glu Ser Arg Leu
91           35           40           45
93 Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln Met Lys Ala Arg Glu
94           50           55           60
96 Met Gln Lys Gln Arg Ala Gln Gly Ser Gly Ile Ser Val Gln Lys Arg
97   65           70           75           80
99 Ser Cys Asn Thr Ala Thr Cys Met Thr His Arg Leu Val Gly Leu Leu
100           85           90           95
102 Ser Arg Ser Gly Ser Met Val Arg Ser Asn Leu Leu Pro Thr Lys Met
103           100          105          110
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112 <213> ORGANISM: Sus sp.
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115 <221> NAME/KEY: CDS
116 <222> LOCATION: (1730)..(1815)
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120 <222> LOCATION: (2323)..(2457)
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124 <222> LOCATION: (2754)..(2910)
126 <400> SEQUENCE: 5
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131 aaccgcactt ggacatggta gtcttagggg accggggatg ccttgtaatg ctggactctg 180
133 ctctacaaag atcacatagc tggggatgga gagggatgtg agcctgcgaa accgaacagg 240

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135 taaagttttac catgacgtca aactgtcctt aaattcctgc tcactttgcg tgtgtttttc 300
137 gttggtgccc accaacctcc ccacccctc ccaccccgcc catcaatgac ctcaatgcaa 360
139 atacaagtgg ggtggtcctg ttggatgctc caggttctgg acgcaagtag tgacacaatc 420
141 ctggggctca ggatctttcc tctcattggt tgcctggagc tctgggacca cccagattc 480
143 agagcggcgg gaataagagc agctgctggt gcggggaagg gttagaggca ctaccacct 540
145 caagtgtctc tgccgcttct tccacagtgc catcgctga cgccaacgct gctgcctctg 600
147 ctccctctc tgctccagtc cacctgggtc ctgctgccc gtaagcccgg agattcctgc 660
149 taagctgtgg ttctgtttct ctctccctct cctcccttcc ctctctctcc attggatttt 720
151 cttagctgat ctcttttccc gtctcaaatg tcctgtccac ttctctctgg gtctcttcat 780
153 cctgtaatat gccttactgc gcaattcatt ctaggtcctt ttcacaggta actctggatg 840
155 gtctcagttc ggggattccc tgctctactc ttctgagct gagctgggct ccagtcttgt 900
157 ccccgagca gagctgctta ggtccgtggt gggattttgg agctctccag gcacttcagg 960
159 gagaggagga tgcaggaata gctttgagca gaagaaactt tcatggatcc catctcctct 1020
161 tacctacaag gatcgctgga aatggggctg ttaaagcga cagtgcgaat ggggtggcaa 1080
163 taggtgcaat gactgagggg aaagtagcta ttaaagcga cagtgcaaat ggggtggcaa 1140
165 gaactcccc tcccgaccg ccacccatt taatcttggg tcccaattta aggctgtacc 1200
167 agcttgtttc ttacagggtg ctctttgcca gagtatggag cagctggaca gtaaaatttg 1260
169 gttcttcagt ttctcaggga ttccaactgc agagatatgt cctcccaact ccccttcccc 1320
171 ccagccaggt ataagcaaaa atcaggcatc aggagagatg ctgatgggtt gcactatggg 1380
173 aaaagctgtg gtgacaggta ctgcgagtct gtcctccagg agtcccggcc aacaggttga 1440
175 aggtgagagt tgggtgtgct tgggcagggg gctatggacg gagacctcct caccagttg 1500
177 tcctgctagg ctcttttgct aaaccaaaca tgttgaggc tcaactggatc ttccagcagt 1560
179 ccacttggct gaggaggaaa tgatggtgaa aggaaaggac acgagcagcc tgaagccagg 1620
181 aagccaggga gttggaggca gaggcaggag cagagcccag gtctgtgggc tcaatgaact 1680
183 tggaaactgct acaggtggtg acattgttct tcccttgca aggggcacc atg ggc ttc 1738
184 Met Gly Phe
185 1
187 tgg aaa ttt ccg ccc ttc ctg gtt ctc agc atc ctg gtc ctg tac cag 1786
188 Trp Lys Phe Pro Pro Phe Leu Val Leu Ser Ile Leu Val Leu Tyr Gln
189 5 10 15
191 gca ggc atg ttc cac aca gca cca atg ag gtaagacagc cctgccaaaca 1835
192 Ala Gly Met Phe His Thr Ala Pro Met Arg
193 20 25
195 agcacactca cttgatgaga atgtaataa aacgtgtata taaatttatt ataaggtggc 1895
197 tctgtagaac aatggatagt gccttgogct cctataagtt tatcataagc tttatgtgta 1955
199 cacaaagttt gtaaataagac ataagatata cagtactcat gattgtaaat tttatataac 2015
201 ttatcaaacc tcacagcatg cttttttggt ttcatcaaat atttgtacct ttagcacacg 2075
203 tatatgctca tattaccata atttaagaaa tggattgtat ccaatttgcc aaatactttg 2135
205 ctagtaaaatt tgttattaaa tctgatatgg gatctacaca tctcattttt caccttcatt 2195
207 caaactgcat taagctaaaa ttattttccc attcaacta tcagaaacca ggcaacctgg 2255
209 ctgtttatcc tggggagggg caggcaggag atcagaacct gtttttaggc ttgcttcccc 2315
211 tccttag g tct gcc ttt ggg agc cct ttt gat cct gct acc ctc tct gag 2365
212 Ser Ala Phe Gly Ser Pro Phe Asp Pro Ala Thr Leu Ser Glu
213 30 35 40
215 gag gaa tca cgc ctc ctt ttg gct gca atg gtg aat gac tat gag cag 2413
216 Glu Glu Ser Arg Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln
217 45 50 55
219 atg aag gcc cgt gag atg cag aag cag agg gca cag ggc tcc gg 2457
220 Met Lys Ala Arg Glu Met Gln Lys Gln Arg Ala Gln Gly Ser Gly

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221 60          65          70
223 gtaaggttcc ctgccaagg acaacagggc atccctttct tcctctggtc aggcccagga 2517
225 aggcataattt taaagtcact tttagagtttt ctgacccccc tggacatgtc tgtgggatga 2577
227 ttatggcattt tcccctgacg gcctaggatt ttctgctgtg atgacctttt ctagcagaaa 2637
229 tactcaaggt tcaactggtcc tctcaaggca gtagtcttcc atgacgattc tgtcgtacag 2697
231 cacctgcact caacctctca ctgacggggc ttttctttct ttatcccaca aatcag c 2754
233 atc agt gtc cag aag aga tcc tgc aac act gcc acc tgc atg acc cat 2802
234 Ile Ser Val Gln Lys Arg Ser Cys Asn Thr Ala Thr Cys Met Thr His
235 75          80          85          90
237 cgg ctg gtg ggc ttg ctc agc aga tct ggg agc atg gtg agg agc aac 2850
238 Arg Leu Val Gly Leu Leu Ser Arg Ser Gly Ser Met Val Arg Ser Asn
239          95          100          105
241 ctg ttg ccc acc aag atg ggc ttc aaa gtc ttt ggt ggg cgc cgc agg 2898
242 Leu Leu Pro Thr Lys Met Gly Phe Lys Val Phe Gly Gly Arg Arg Arg
243          110          115          120
245 aac ttt tgg atc tgagcagtgg gatgattcca ggaggaaggt gactgccctt 2950
246 Asn Phe Trp Ile
247          125
249 tttgtacctt cgggtgggag gacagaggac tgggtattgc aggggtgcat tccacacctt 3010
251 aaccctctgt gagcgcatgg gggtaaaacc tccacatggc aagggtgcca caccagtgtc 3070
253 tggagaaagg actgataatc cctataactg aaacattggg ctctttctct ctgtttctcc 3130
255 agtctctccc tgtgacactg acatcatctg ccaggaaata tagacctgtt ttacttaaaa 3190
257 cactgttccc tgggtattaa ttgggggtcca gctctagcat tagaatttga aaggtaatga 3250
259 ccctaccttt ttggagcata ccttacaatg ttatgaactt ggagcataga ctcggtattca 3310
261 aatactgtgt ctgtcttcca ctaactgtga ccataggcaa gtatgcctct gagcctcagc 3370
263 ttctccttgt aacttgaagg caacaatagt atcctcaata taaaaattaa ttagtataac 3430
265 atatgacaag agcctgttaa ctaagaatta ataacattct gttacttttt tccctcctag 3490
267 gttactatga ctctgaactc tacttcgttt aatttacaat gaaagcaacc tactaaaaaa 3550
269 tagcatggaa gacatccatg tatgcatgct tctggaaact gaaaacactc ttttccttga 3610
271 aataaaactaa aactaaatgc aaaataaaat caatgcatca atgcagttac cttgtgtgca 3670
273 tcttttgtgt atatgattct ataatatgat gcatgtctca ttaggtttaa tggtagcaaa 3730
275 tctggccccct gtcagccaac ctgttggtgg gggcagctct gctaaacctc aggggtcacat 3790
277 gaattc 3796
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281 <211> LENGTH: 40
282 <212> TYPE: PRT
283 <213> ORGANISM: Bos sp.
285 <400> SEQUENCE: 6
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287 1          5          10          15
289 Ser Arg Ser Gly Ser Met Val Arg Ser Asn Leu Leu Pro Thr Lys Met
290          20          25          30
292 Gly Phe Lys Ile Phe Asn Gly Pro
293          35          40
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 649
298 <212> TYPE: DNA
299 <213> ORGANISM: Bos sp.
301 <400> SEQUENCE: 7

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## RAW SEQUENCE LISTING

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302 tgtctctgcc acttctgcc gactgccact gctgtctgcc aaagctactg ctgtctgtcc 60
303 ttctctctgct cccagccacc tgggtgccgc tgctcagagag gtgtcatggg cttctggaag 120
304 ttccccccat tcttggtcct cagcatcctg gtcttgtagc aggcaggcat gtttcatgca 180
305 gcaccattca ggtctgtcct tgatgggcgt ttgatcctg ctaccctgga tgaggaggaa 240
306 tcgcgcctcc tactggctgc gatggtgaat gactacgagc agatgagggc ccgggagtcg 300
307 gagaaggctc agaagaccga gggctcccgc atccagaaga gagcctgcaa cactgccacc 360
308 tgcattgaccc atcgcttggc aggtctggctg agcagatctg ggagtatggt gaggagcaac 420
309 ttgtctgccga ccaagatggg tttcaagatc ttcaatgggc cccgcaggaa ctctgtggtt 480
310 taaacagtga aatgacgctg ggaataaggt caccaggaag ctgaactcta cttttagttt 540
311 gcatgaaggc acctacaaa aaaagaaaat agcatggaag atacccatgt atgcatgctt 600
312 ctcgatattg aaaacattct tcttttcctt gaaataaact aaatgcaga 649

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316 &lt;211&gt; LENGTH: 125

317 &lt;212&gt; TYPE: PRT

318 &lt;213&gt; ORGANISM: Bos sp.

320 &lt;400&gt; SEQUENCE: 8

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322   1           5           10           15
324 Leu Tyr Gln Ala Gly Met Phe His Ala Ala Pro Phe Arg Ser Val Phe
325           20           25           30
327 Asp Gly Arg Phe Asp Pro Ala Thr Leu Asp Glu Glu Glu Ser Arg Leu
328           35           40           45
330 Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln Met Arg Ala Arg Glu
331           50           55           60
333 Ser Glu Lys Ala Gln Lys Thr Glu Gly Ser Arg Ile Gln Lys Arg Ala
334           65           70           75           80
336 Cys Asn Thr Ala Thr Cys Met Thr His Arg Leu Ala Gly Trp Leu Ser
337           85           90           95
339 Arg Ser Gly Ser Met Val Arg Ser Asn Leu Leu Pro Thr Lys Met Gly
340           100          105          110
342 Phe Lys Ile Phe Asn Gly Pro Arg Arg Asn Ser Trp Phe
343           115          120          125

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346 &lt;210&gt; SEQ ID NO: 9

347 &lt;211&gt; LENGTH: 38

348 &lt;212&gt; TYPE: PRT

349 &lt;213&gt; ORGANISM: Canis sp.

351 &lt;400&gt; SEQUENCE: 9

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352 Ser Cys Asn Ser Ala Thr Cys Val Ala His Trp Leu Gly Gly Leu Leu
353   1           5           10           15
355 Ser Arg Ala Gly Ser Val Ala Asn Thr Asn Leu Leu Pro Thr Ser Met
356           20           25           30
358 Gly Phe Lys Val Tyr Asn
359           35

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362 &lt;210&gt; SEQ ID NO: 10

363 &lt;211&gt; LENGTH: 686

364 &lt;212&gt; TYPE: DNA

365 &lt;213&gt; ORGANISM: Canis sp.

367 &lt;400&gt; SEQUENCE: 10

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368 tctgccacat ccacgggtgcc atcgcttgac atcgagcgcc aacactgcc cagctgccgc 60

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; N Pos. 9,12,15

Seq#:32; N Pos. 6,15

Seq#:33; Xaa Pos. 2,7

Seq#:34; Xaa Pos. 2,7

## VERIFICATION SUMMARY

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L:1361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0  
L:1384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0  
L:1403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0  
L:1426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0